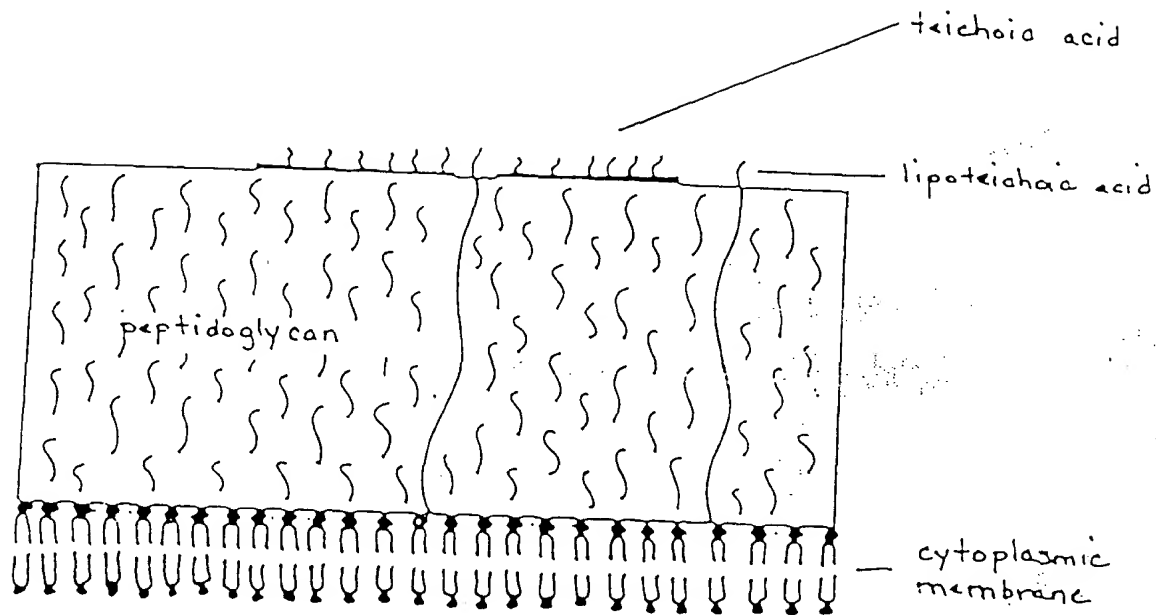
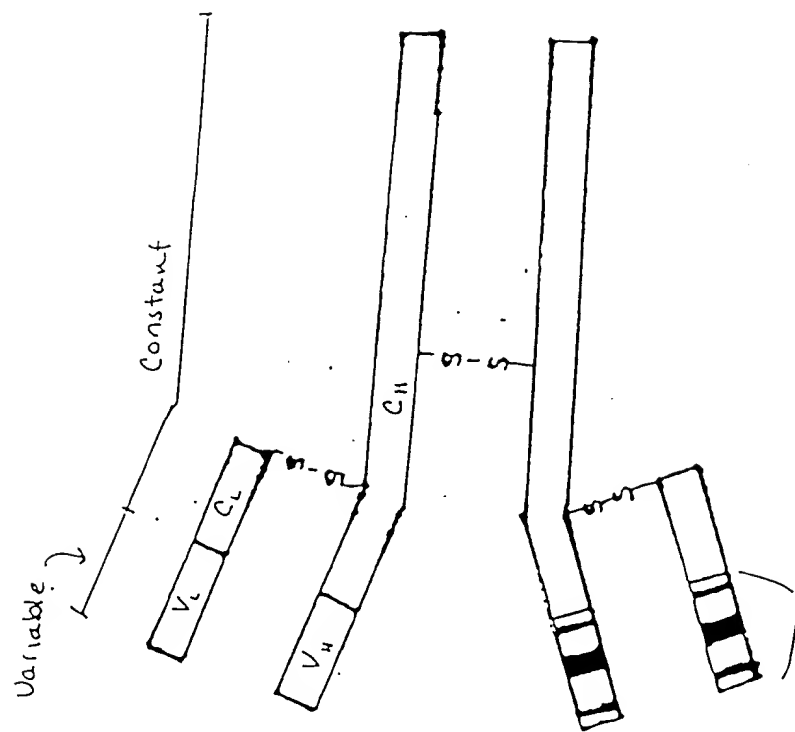


FIGURE 1



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FIGURE 2



Hypervariable regions  
Containing 3 CDRs

FIGURE 3

Effect of Anti-Staph MAB 96-110 on  
Survival in a Lethal *S. aureus* Sepsis Model

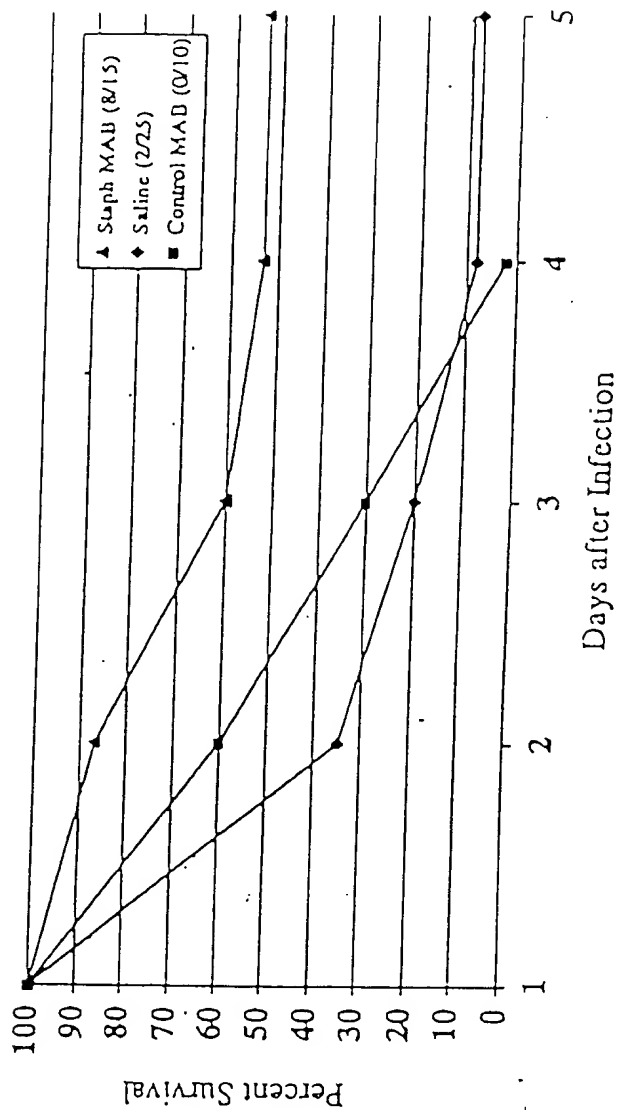


FIGURE 4

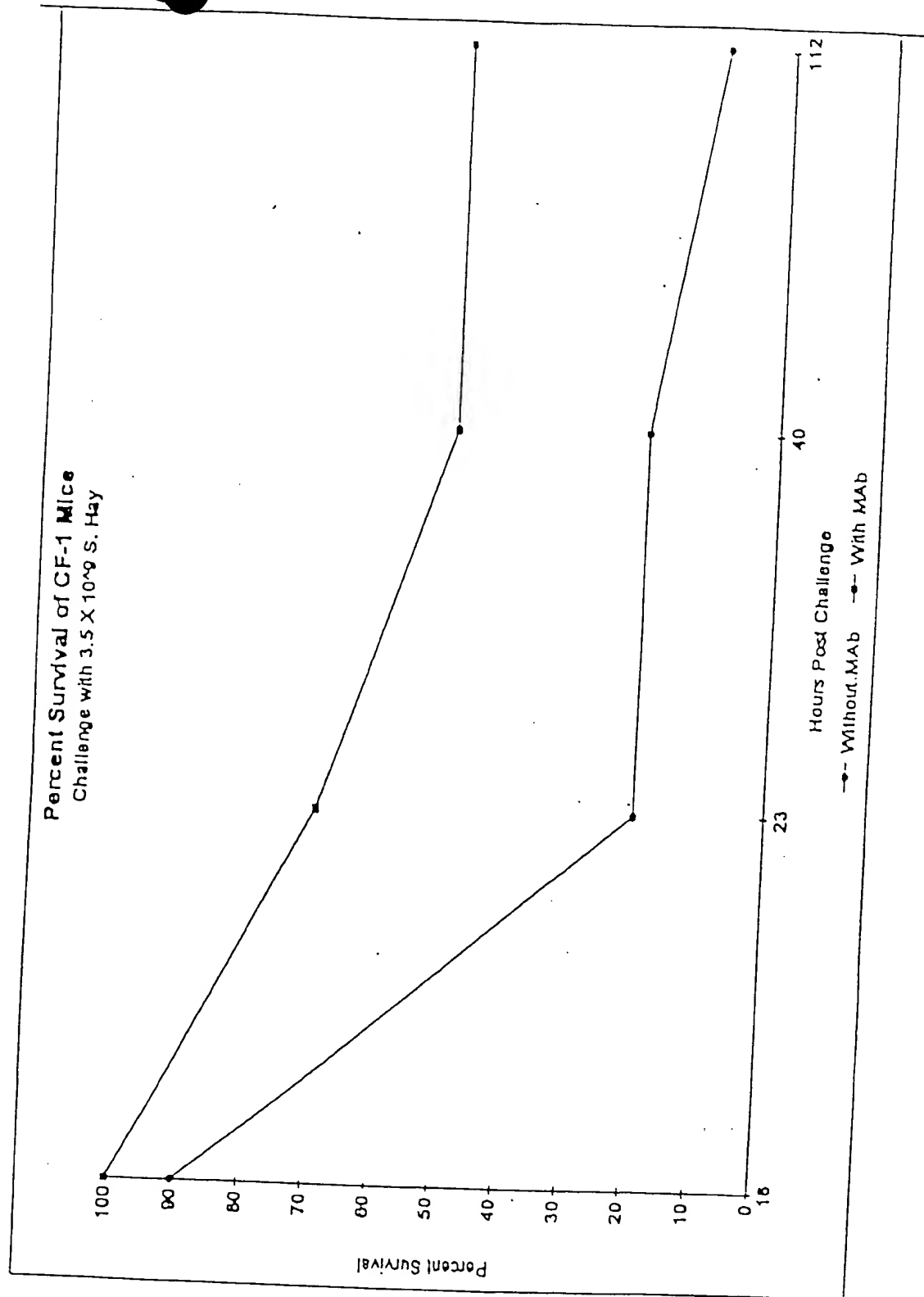


FIGURE 5

6MER_SEQ		10	20	30	
11	13.6mer2-1	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	SEQ ID NO. 4
61		C A H	A D R V	Y G A	SEQ ID NO. 5
12	14.6mer2-2	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
65		C A H	A D R V	Y G A	
13	15.6mer2-3	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
66		C A H	A D R V	Y G A	
14	16.6mer2-4	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	SEQ ID NO. 6
62		C A H	A D R V	Y G A	SEQ ID NO. 7
15	17.6mer2-5	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
67		C A H	A D R V	Y G A	
16	18.6mer2-6	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
68		C A H	A D R V	Y G A	
17	19.6mer2-7	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
69		C A H	A D R V	Y G A	
18	20.6mer2-8	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
70		C A H	A D R V	Y G A	
19	21.6mer2-9	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
71		C A H	A D R V	Y G A	
20	22.6mer2-10	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
72		C A H	A D R V	Y G A	
21	23.6mer2-11	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
73		C A H	A D R V	Y G A	
22	24.6mer2-12	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
74		C A H	A D R V	Y G A	
23	25.6mer2-13	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
75		C A H	A D R V	Y G A	
24	26.6mer2-14	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
76		C A H	A D R V	Y G A	
25	27.6mer2-15	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
77		C A H	A D R V	Y G A	
26	28.6mer2-16	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
78		C A H	A D R V	Y G A	
27	29.6mer2-17	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
79		C A H	A D R V	Y G A	
28	30.6mer2-18	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
80		C A H	A D R V	Y G A	

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FIGURE 6

09893615-062901

15MER2.SEQ		10	20	30	40	50	60
50	07.15mer2-1/0	GGGGCTTGGC	ATTGGCGTCA	TGGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 8
70		G A W	H W R H	R I P	L Q L	A A G R	G A SEQ ID NO. 9
52	09.15mer2-3/0	GGGGCTTGGC	GGCATGGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 10
72		G A R	R H G N	F S H	F F H	R S L I	G A SEQ ID NO. 11
53	10.15mer2-4/0	GGGGCTTGGC	GGGTTTCTT	TATTCATCT	TATCGTCTC	GGGGTTCGGC	TGGGGCC SEQ ID NO. 12
73		G A W	K A L F	S H S	Y R P	R G S A	G A SEQ ID NO. 13
54	11.15mer2-5/0	GGGGCTAGGC	ATTGGCGTCA	TGGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 14
74		G A R	H W R H	R I P	L O L	A A G R	G A SEQ ID NO. 15
56	13.15mer2-7/0	GGGGCTTGGC	ATTGGCGTCA	TGGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 16
76		G A W	H W R H	R I P	L O L	A A G R	G A SEQ ID NO. 17
57	14.15mer2-8/0	GGGGCTTGGC	ATTGGCGTCA	TGGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 18
77		G A W	H W R H	R I P	L O L	A A G R	G A SEQ ID NO. 19
58	15.15mer2-9/0	GGGGCTCAGC	TGGCTGTTT	CTATCCCTCT	TTGCTGATC	CTACTGACCT	TGGGGCC SEQ ID NO. 20
78		G A Q	V A V L	Y P P	L A D	A T E L	G A SEQ ID NO. 21
59	16.15mer2-10/0	GGGGCTCGTC	GGCATGGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 22
79		G A R	R H G N	F S H	F F H	R S L I	G A SEQ ID NO. 23
60	17.15mer2-11/0	GGGGCTCGTC	GGCATGGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 24
80		G A R	R H G N	F S H	F F H	R S L I	G A SEQ ID NO. 25
61	18.15mer2-12/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 26
81		G A W	R M Y F	S H R	H A H	L R S P	G A SEQ ID NO. 27
62	19.15mer2-13/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 28
82		G A W	R H Y F	S H R	H A H	L R S P	G A SEQ ID NO. 29
63	20.15mer2-14/0	GGGGCTTGGC	GGAGTATTT	TTCTATCAT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 30
93		G A W	R K Y F	S Y H	H A H	L C S P	G A SEQ ID NO. 31
64	21.15mer2-15/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 32
94		G A W	R M Y F	S H R	H A H	L R S P	G A SEQ ID NO. 33
65	22.15mer2-16/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 34
95		G A W	R H Y F	S H R	H A H	L R S P	G A SEQ ID NO. 35
66	23.15mer2-17/0	GGGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 36
96		G A W	R H Y F	S H R	H A H	L R S P	G A SEQ ID NO. 37
67	24.15mer2-18/0	GGGGCTCGTC	GGCATGGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 38
97		G A R	R H G N	F S H	F F H	R S L I	G A SEQ ID NO. 39
68	25.15mer2-19/0	GGGGCTTGGC	ATTGGCGTCA	TGGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 40
98		G A W	H W R H	R I P	L Q L	A A G R	G A SEQ ID NO. 41
69	26.15mer2-20/0	GGGGCTCGTC	GGCATGGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 42
99		G A R	R H G N	F S H	F F H	R S L I	G A SEQ ID NO. 43

FIGURE 7

15mer1 SEQ		10	20	30	40	50	60	
1	28.15mer1-2	GGGGCTGATT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	SEQ ID NO. 44
17		C A D	W I T F	H R R	H H D	R V L S	G A	SEQ ID NO. 45
2	29.15mer1-3	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	SEQ ID NO. 46
18		C A C	W I T F	H R R	H H D	R V L S	G A	SEQ ID NO. 47
5	32.15mer1-6	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
11		C A G	W I T F	H R R	H H D	R V L S	G A	
2	33.15mer1-7	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
16		C A G	W I T F	H R R	H H D	R V L S	G A	
3	34.15mer1-8	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
17		C A G	W I T F	H R R	H H D	R V L S	G A	
4	35.15mer1-9	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
18		C A C	W I T F	H R R	H H D	R V L S	G A	
5	36.15mer1-10	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
19		C A G	W I T F	H R R	H H D	R V L S	G A	
6	37.15mer1-11	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
10		C A C	W I T F	H R R	H H D	R V L S	G A	
7	38.15mer1-12	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
11		C A C	W I T F	H R R	H H D	R V L S	G A	
8	39.15mer1-13	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
12		C A C	W I T F	H R R	H H D	R V L S	G A	
9	20.15mer1-14	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
13		C A G	W I T F	H R R	H H D	R V L S	G A	
0	21.15mer1-15	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
14		C A G	W I T F	H R R	H H D	R V L S	G A	
1	22.15mer1-16	GGGGCTGGGA	AGGCTATGTT	TATCGTATCT	TATCGTATCT	GGGGTTCGGC	TGGGGCCC	SEQ ID NO. 48
15		G A G	K A M F	S H S	Y R H	R G S A	G A	SEQ ID NO. 49
2	23.15mer1-17	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
16		C A C	W I T F	H R R	H H D	R V L S	G A	
3	24.15mer1-18	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
17		C A C	W I T F	H R R	H H D	R V L S	G A	
4	25.15mer1-19	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
18		C A G	W I T F	H R R	H H D	R V L S	G A	
5	26.15mer1-20	GGGGCTGGTT	GGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCCC	
19		C A G	W I T F	H R R	H H D	R V L S	G A	

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FIGURE 8

masterlist		10	20	30	40	50	60	70	
54	15mer 1st.1	GGGCTGATT	GGATTACTTT	TCATCTGCTT	CATCATGATC	CTCTTCTTTC	TCGGCCCC	16/17	SEQ ID NO 50
57		G A D	W I T F	H R R	H H D	R V L S	G A		SEQ ID NO 51
90	15mer 1st.2	GGGCTTAGTC	GTATATATCT	TCCTCTGCTG	TCGCTTTTCC	TTCTCTTCTC	TCGGCCCC	1/10	SEQ ID NO 52
91		G A S	R H M L	A R W	S R L	L A V P	G A		SEQ ID NO 53
71	15mer 1st.16	GGGCTTGGGA	AGGCTATGTT	TAGTCATTCT	TATCTTCATC	GGGCTTCGCC	TCGGCCCC	1/17	SEQ ID NO 54
85		G A G	K A M F	S H S	Y R H	R G S A	G A		SEQ ID NO 55
92	15mer 2nd.1	GGGCTTTGGC	ATTGGCGTCA	TCGTATTCTT	CTTCAGCTTC	CTCTCTGCTC	TCGGCCCC	5/18	SEQ ID NO 56
98		G A W	H W R H	R I P	L O L	A A G R	G A		SEQ ID NO 57
93	15mer 2nd.3	GGGCTCTGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCTTTCAT	TCGGCCCC	1/18	SEQ ID NO 58
99		G A R	R H G N	F S H	F F H	R S L I	G A		SEQ ID NO 59
94	15mer 2nd.4	GGGCTTTGGA	AGGCTTTGTT	TAGTCATTCT	TATCTCTCTC	GGGCTTCGCC	TCGGCCCC	1/18	SEQ ID NO 60
100		G A W	X A L F	S H S	Y R P	R G S A	G A		SEQ ID NO 61
95	15mer 2nd.9	GGGCTCAGC	TCGGCTTTT	GTATCTCTCT	TTGGCTGATC	CTACTGAGCT	TCGGCCCC	1/18	SEQ ID NO 62
101		G A Q	V A V L	Y P P	L A D	A T E L	G A		SEQ ID NO 63
96	15mer 2nd.12	GGGCTTTGGC	GTATCTATTT	TTCTCATCTG	CACTGGCCATC	TTCTCTAGTCC	TCGGCCCC	1/18	SEQ ID NO 64
102		G A W	R M Y F	S H R	H A H	L R S P	G A		SEQ ID NO 65
97	6mer 2nd.1	GGGCTCATC	CGATAGGCT	TTATCGGGCC				15/18	SEQ ID NO 66
103		G A H	A O R V	Y G A					SEQ ID NO 67

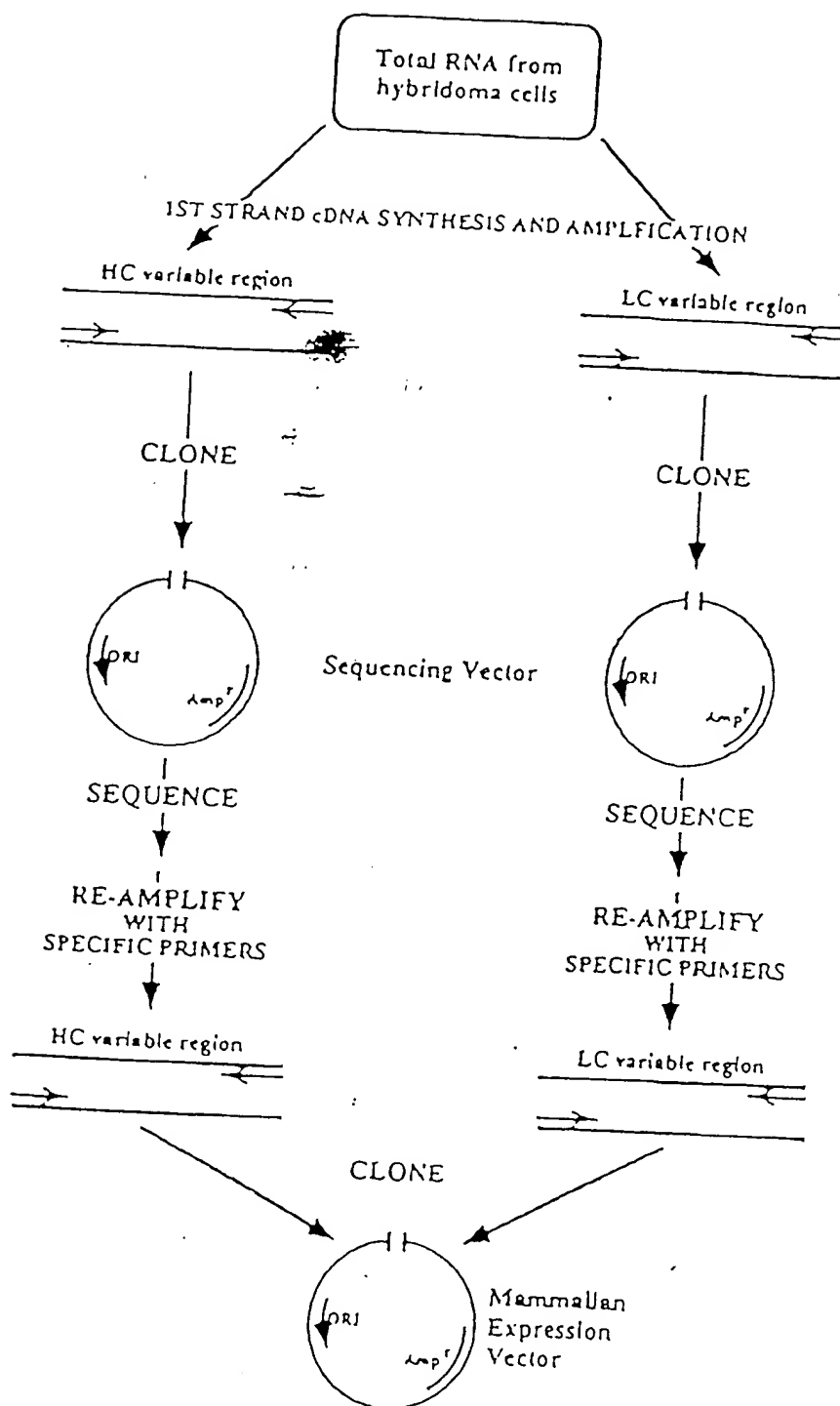


FIGURE 9

Comparison of Signals at  $6.25 \times 10^{11}$  vir/mL.



FIGURE 10: General Cloning Strategy



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FIGURE 11

*Mouse Heavy Chain "front" primers*

JSS1  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGARGTRMAGCTKSAXGAGWC-3' SEQ ID NO 68  
JSS2  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGARGTYCARCTKCARCARYC-3' SEQ ID NO 69  
JSS3  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGAGGTGAAGCTKSTSGARTC-3' SEQ ID NO 70  
JSS4  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGAVGTGMWGCTKGTGGAGWC-3' SEQ ID NO 71  
JSS8  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGAGGTBCARCTKMARSARTC-3' SEQ ID NO 72

*Mouse Heavy chain "back" primers*

JS160  
5'-GCTGCCACCGCCACCTGMRGAGACDGTGASTGARG-3' SEQ ID NO 73  
JS161  
5'-GCTGCCACCGCCACCTGMRGAGACDGTQASMOTRG-3' SEQ ID NO 74  
JS162  
5'-GCTGCCACCGCCACCTGMRGAGACDGTGASCAGRG-3' SEQ ID NO 75

*Mouse Light Chain Leader "front" primers*

PMC12  
5'-CCCGGGCCACCATGGAGACAGACACACTCCTG-3' SEQ ID NO 76  
PMC13  
5'-CCCGGGCCACCATGGATTTTCAAGTCCAGATTTTC-3' SEQ ID NO 77  
PMC14  
5'-CCCGGGCCACCATGGAGWCACAKWCTCAGGTC-3' SEQ ID NO 78  
PMC15  
5'-CCCGGGCCACCATGKCCCCWRCTCAGYTTCTKG-3' SEQ ID NO 79  
PMC55  
5'-CCCGGGCCACCATGAAGTTGCCTGTTAGGCTG-3' SEQ ID NO 80

*Mouse Light Chain "back" primer*

OKA57  
5'-GCACCTCCAGATGTAACTGCTC-3' SEQ ID NO 81

*"96-110" Specific Primers*

96110HF2  
5'-TAATATCGCGACAGCTACAGGTGTCCACTCCCGAAGTGATGCTGGTGGAGWCTG-3' SEQ ID NO 82  
96110HB  
5'-TTATAGAAATTCGTGAGGAGACGGTGAGTGAG-3' SEQ ID NO 83  
96110BLF  
5'-TTAGGCGATATCTGTTCTCTCCCACTCTCC-3' SEQ ID NO 84  
96110BLB  
5'-GTAACCGTTCCGAAAGTGTAAGTACGTTTATTTCCAGCATGCTCC-3' SEQ ID NO 85

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FIGURE 12

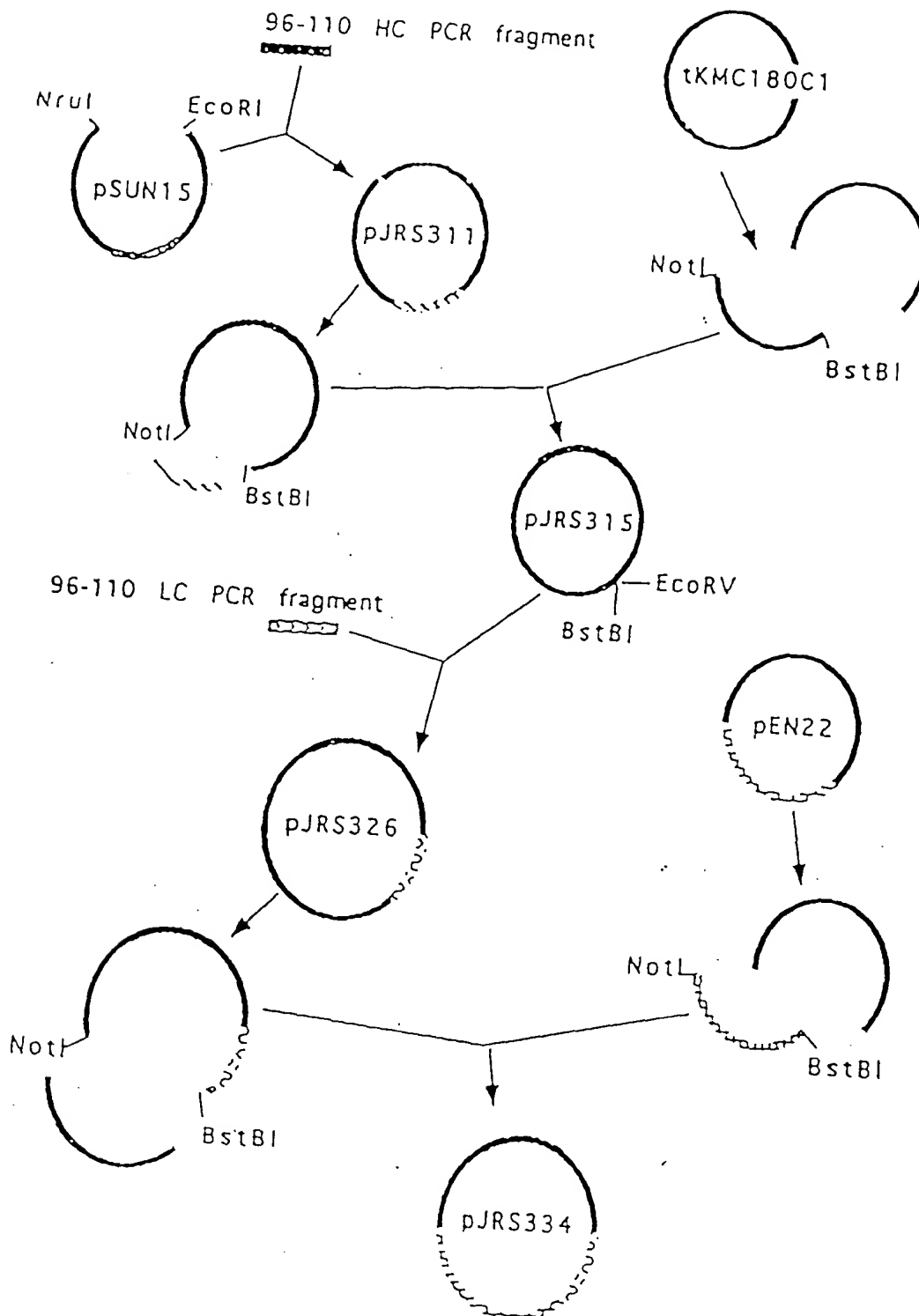
96-110 anti-staph (HAY) heavy chain variable region (type IIIA)

CAAATGCTGCTGGTGGAGGATTCGTCAGCCTAAAGGGTCATTGAACTCTCATGTGTCAGCCTCTGGATTCACTTCAAT SEQ ID NO. 86  
 EVHLVBSGGGLVQPXGSLKLSCLASGFTPH SEQ ID NO. 87  
AACTAGCCCATGAAAT TGGCTCCGCCAGGCTCCAGGAAGGGTTTGGAAATGGGTGCT SEQ ID NO. 88  
 NYAHN WVRQAPEGKGLBHWVA SEQ ID NO. 89  
CCCATAGAGAACTAAAGTAAATATAGCAACATTTATACCAATTCAGTGAAGAC SEQ ID NO. 90  
 RIRSKSNHYATPYADSVXD SEQ ID NO. 91  
 AGGTTACCAATCTCCAGATGATTCACAAAGCATGCTCTATCTGCAATGAACTGAAAGGACAGCAGCCATGTATTCTGTCTGACAG SEQ ID NO. 92  
 RFTISRDSDSQSHLYLQLQHNNLKTXBTATAYCYCVR SEQ ID NO. 93  
CGGCGGCTTCAGGGATTGACTATGCTATGAGCTAC TGGGTCAAGGAACCTCACTCACTCCCTCTCTCA SEQ ID NO. 94  
 RGLSGIDYAHDDY HGGCGTSLTVSS SEQ ID NO. 95

96-110 anti-staph (HAY) light chain variable region (type VI)

CAAATGCTGCTGCCAGTCTCCAGCAATGCTCTGTCATCTCCAGGGGAAAGGTCAATGACTTGC SEQ ID NO. 96  
 QIVLSQSPALILSLASPGEXKVTHTC SEQ ID NO. 97  
AGGCGCCAGCTCAAGCTTAAATTACATGCA SEQ ID NO. 98  
 RASSSVNYHRS SEQ ID NO. 99  
 TGGTACCAAGCAAGCAGGATCTCCGCCCAAAACCTGGATTCT GCCACATCCAAACCTGGCTTCT SEQ ID NO. 100  
 WYQQKPGSPKPNISATSNLXSS SEQ ID NO. 101  
 GCACTCTCTGCTGCTCACTGAGTGGGTCTGCAACCTCTATCTCTCAATCAAGAGTGGAGCCTCAAGATCTGCCACTTATCTGC SEQ ID NO. 102  
 GVPAPRPSSGSGSGTSGYSLTISRVEXADATYCYC SEQ ID NO. 103  
CAGCACTGGAGTAAACCAACCAAG TTCGAGGGGGGACATGCTGCAATAGCA SEQ ID NO. 104  
 QQWSSSNPPPTFCGGGTMLXIR SEQ ID NO. 105

FIGURE 13



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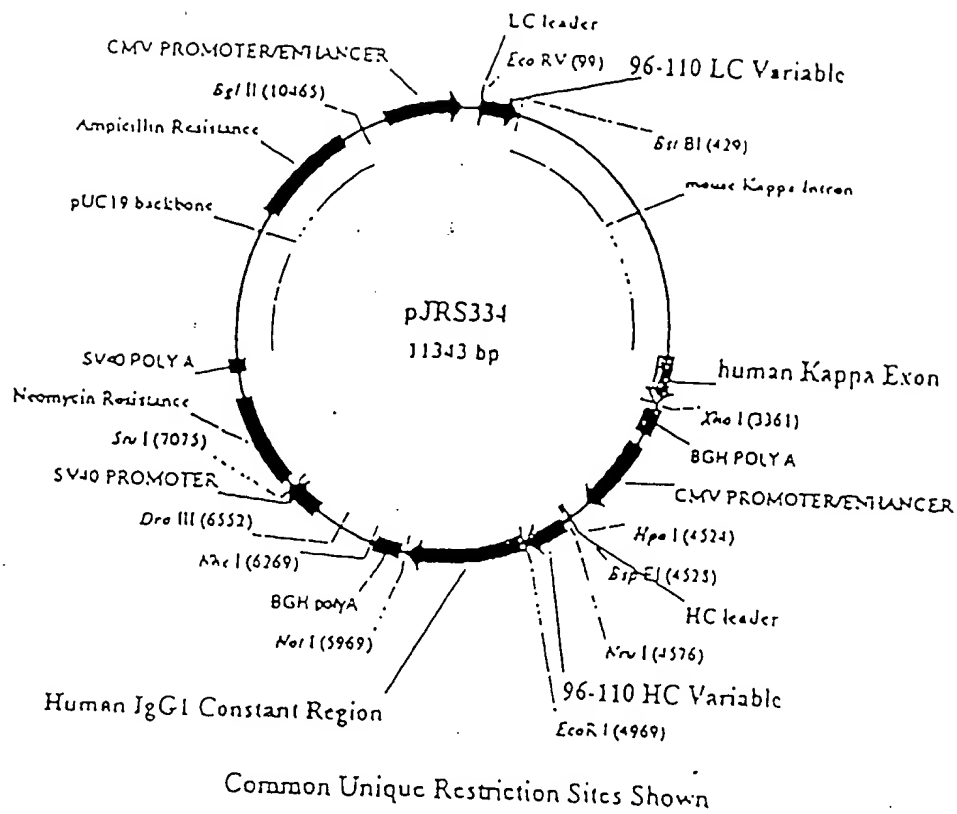
[illegible]

FIGURE 15: Antibody Production ELISA

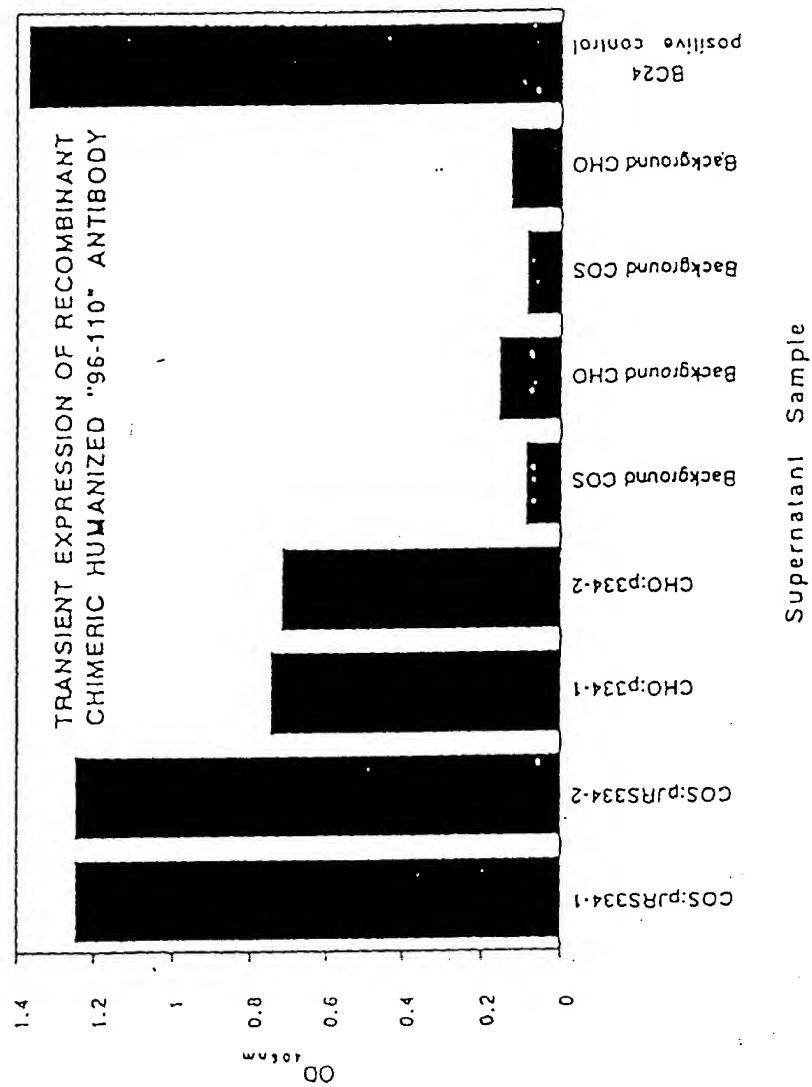
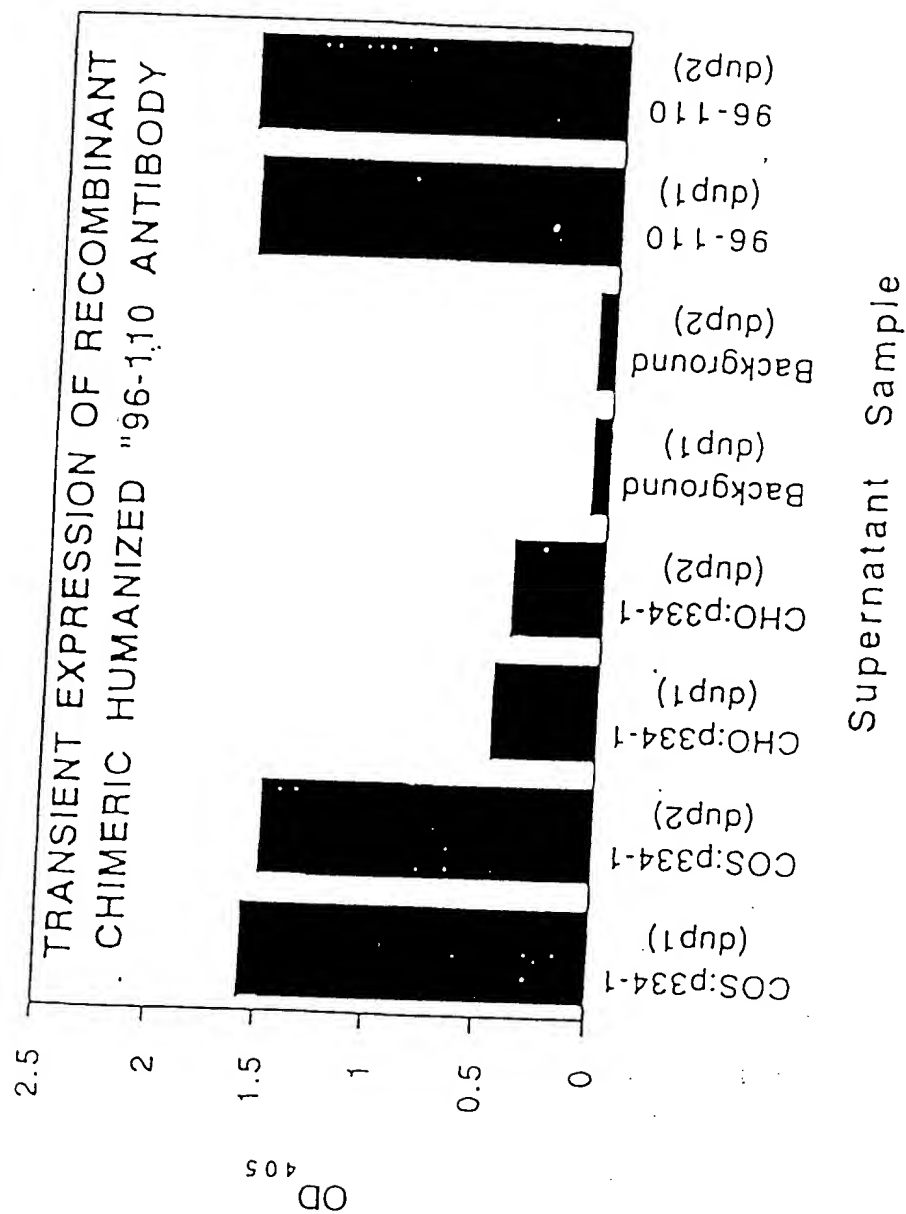
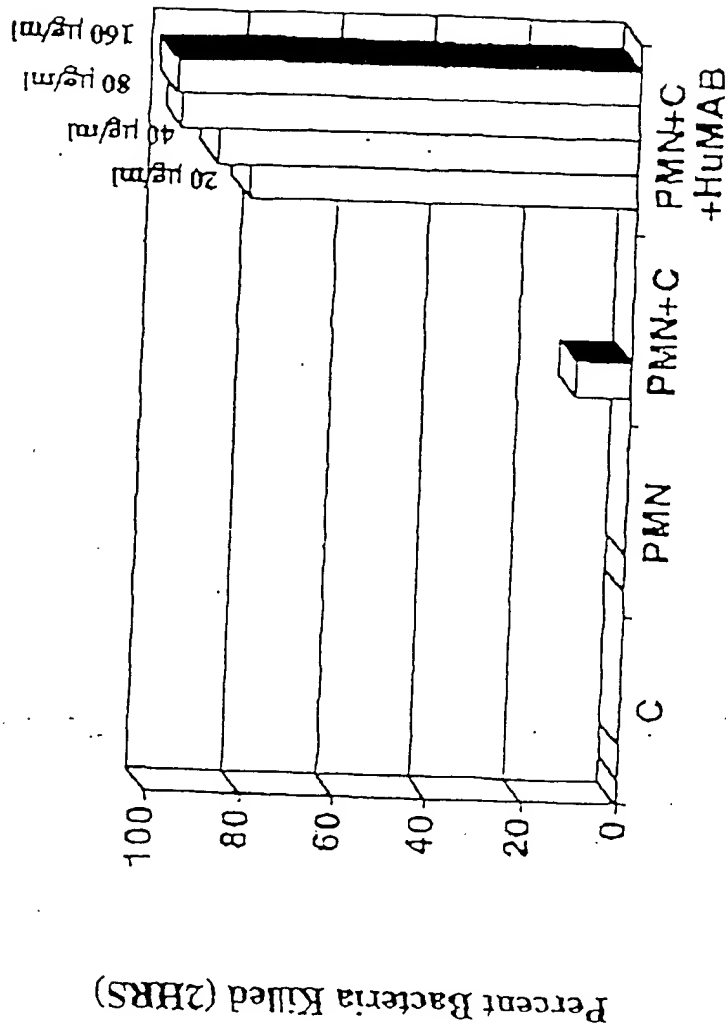


FIGURE 16: Anti-Staph HAY Activity ELISA



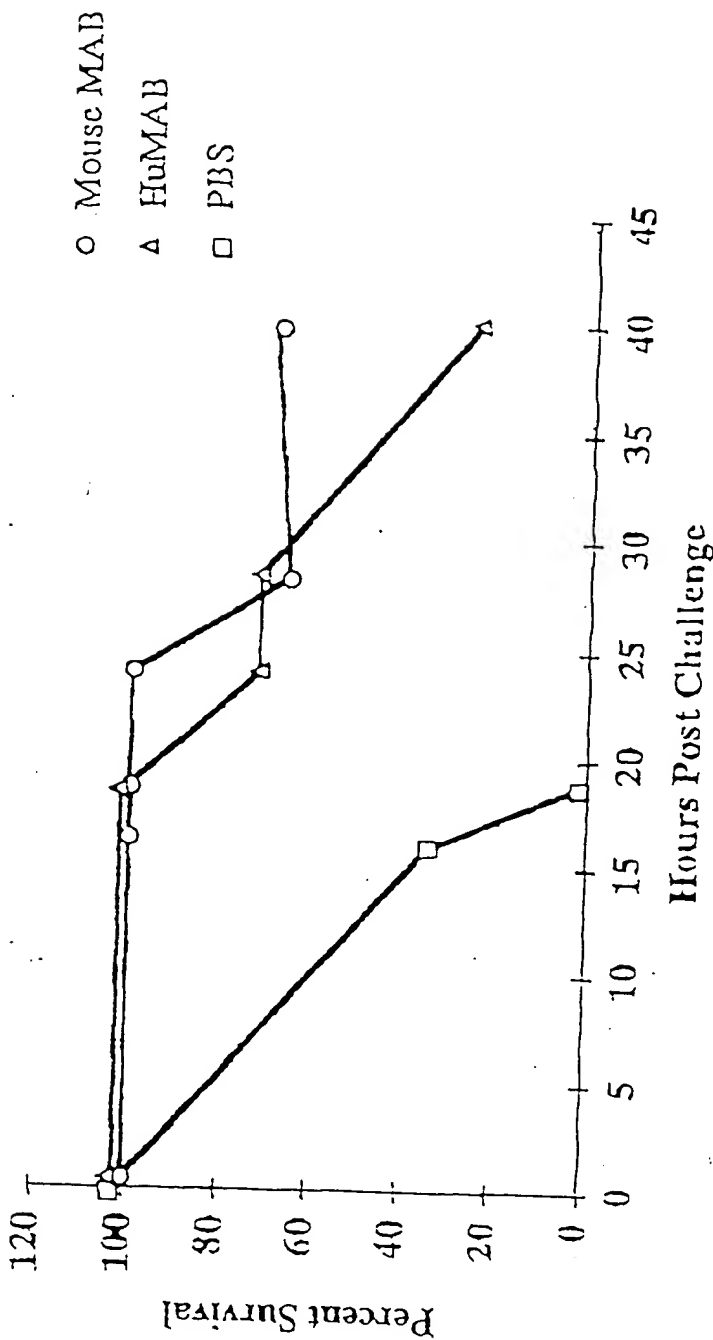


# Opsonic Activity of HuMAB 96-110 for *S.epidermidis* in a Neutrophil Mediated Opsonophagocytic Bactericidal Assay Using Human Complement



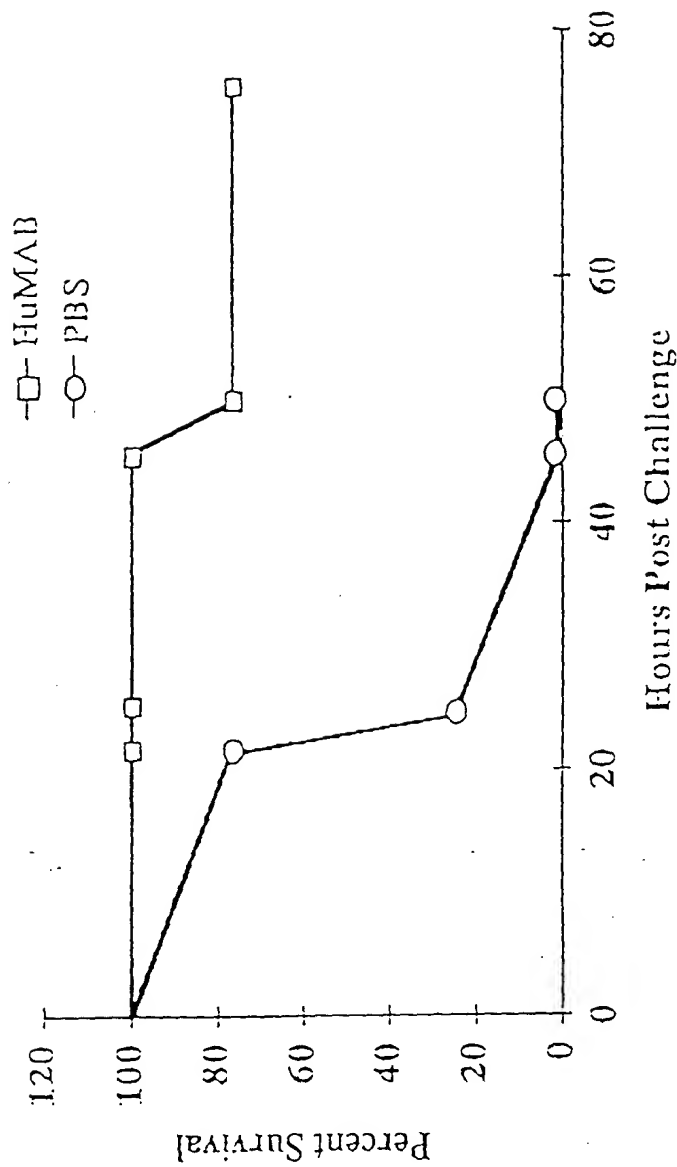
C-Barb-Ex (1:4), Human  
PMN-Human  
Bacterin-*S.epidermidis* (Strain Hay)

# Pilot Study to Compare the Effect of Mouse MAB 96-110 and HuMAB 96-110 in a Lethal Model of *S. Epidermidis* Sepsis



MAB dose: 14 mg/kg given IP, 24 and 1 hour prior to infection

# Survival of CF-1 Mice after Intraperitoneal Challenge with $3 \times 10^9$ *S. epidermidis* (Hay)



18 mg/kg/dose, IP, 24 and 1 Hour prior to infection

# Effect of HuMAB 96-110 on Bacteremia in a Lethal *S. epidermidis* Sepsis Model

Geometric Mean Bacteremia Level

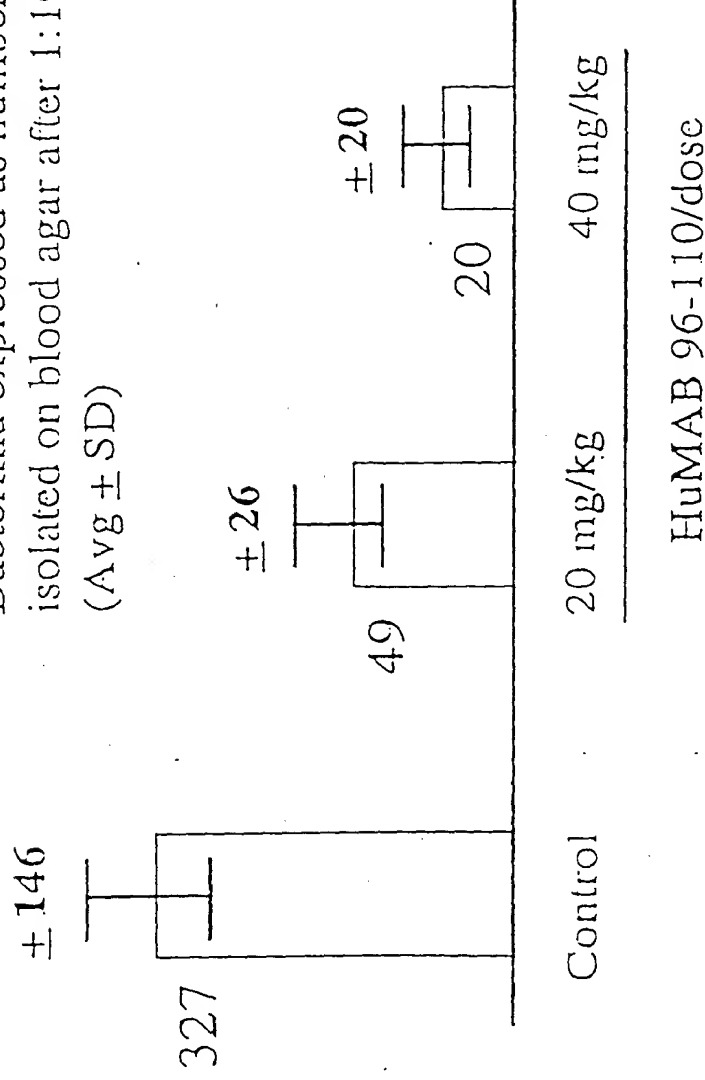
Saline				
Placebo	$6.5 \times 10^4$	$7.2 \times 10^4$	$5.2 \times 10^4$	$7 \times 10^3$
HuMAB				
96-110	$3 \times 10^2$	$7.5 \times 10^2$	$2.1 \times 10^1$	$1.7 \times 10^1$
	4 hrs	8 hrs	12 hrs	18 hrs

Time Post Infection

HuMAB 96-110 18 mg/kg/dose or saline given IP, 24 and 1 hour prior to IP infection with  $3 \times 10^9$  *S. epidermidis* (Hay)

# Bacteremia levels 4 hrs after infection with $3 \times 10^9$ *S.epidermidis*\*

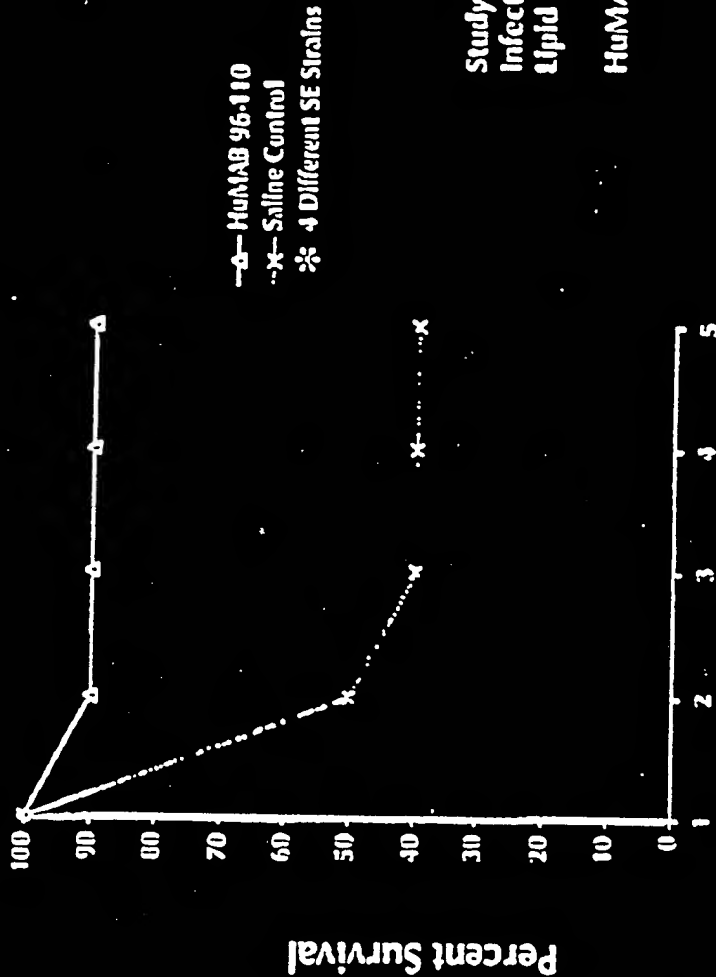
Bactermia expressed as number of bacteria  
isolated on blood agar after 1:1000 dilution  
(Avg  $\pm$  SD)



\* CF-1 mice infected IP with strain Hay-HuMAB given IP x 2

# The Effect of Hu 96-110 on Survival in a Lethal Neonatal *S.epidermidis*\* Sepsis Model: Study II

Survival:  
Hu 96-110 27/30 (90%)  
Saline 12/30 (40%)



## Study II:

Infection--~5x10<sup>7</sup> SE, SQ (with plastic catheter SQ)  
Lipid Emulsion - 0.2 ml, 20% IP day-1 and + 1, 2

doses day 0

HuMAB or Saline- 0.2 ml, IP 30 min before and 24 hrs after infection

Dose: 50-60 mg/kg per dose

Days After Infection

96-110 anti-staph (HAY) heavy chain variable region (type IIIA)

R V H L V H S G C G L V Q P X G G L X L S C A A S G F T P U  
 E A G T G A T G C T G C G A G C A T G C G C A G C C T A A G G G T C A T T G A A C T C T G C A G C C T C T G C A T T C A C C T T C A A T

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

C C C A T A A G A A G T A A A T A A I T A T T G C A A C A T T T T T A T G C C G A T C T C A G T G A A A C A G

AGCTTCA CCA TCTCCAGAGA TGGATTTCACCAATCCATTCATTCATCTGTCATGAG,  
R P T I S R D D S Q S H L Y L Q H N N L X T R D T A H Y Y C V R

U C A S G I D Y A H B X

CCCCCCCCTCACGGCAATGACATATTCCTATTGCAGCTAC TCGGTCCAAAGAACCTCCTCATCTCCCTCTCTCA SEQ ID NO. 867

U C A S G I D Y A H B X

CCCCCCCCTCACGGCAATGACATATTCCTATTGCAGCTAC TCGGTCCAAAGAACCTCCTCATCTCCCTCTCTCA SEQ ID NO. 87

96-110 anti-staph (HAY) light chain variable region (type VI)

Q I V L S O S P A I L S A S P G R K V T H T C  
C A A A T T G T H C T C T C C C A G T C T C A G C A A T C T C T C T C T C A G G T C A C A A T C A C T C T C

3Y35i.Y3Y.f.i.YYY.i.3.i.3Y42I.33Y.33333Y

N A S S V H Y H H

TCGTAACAGCGCAGGAGCGCGAGGCGAGTCCCTCCCGAATTCCT  
 W Y Q Q Q K P G S J P K P W I S  
 A T S W P A A  
 GCGACATCGGACACACGCGCTTCCT

CGA GATGCC C TGCTCCCTTCAG GTCGCGGTC TC GCG C T G Y G L T CTCTCTCAG CAA TCAG CAG C TC GAG C GCTG CAG A TC GCTG CAG A TC A C TCG C

CACACACAGGAGCTATGTAAACCACCCACCG. TTCCGACGGCGGCACACTCCTCGAATTACGA  
O O W S S S H P P T P C C C T U L Z I R SEQ ID NO. 88  
 SEQ ID NO. 89

Can Regions Underlie